

AMENDMENTS TO THE SPECIFICATION:

Please amend the specification as shown:

Please delete the paragraph on page 9, line 14, to page 10, line 1 and replace it with the following paragraph:

The primary amino acid structure may be modified by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like, or by creating amino acid sequence mutants. Covalent derivatives are prepared by linking particular functional groups to TNFR amino acid side chains or at the N- or C-termini. Other derivatives of TNFR include covalent or aggregative conjugates of TNFR or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. For example, the conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast .alpha.-factor leader). TNFR protein fusions can comprise peptides added to facilitate purification or identification of TNFR (e.g., poly-His). The amino acid sequence of TNF receptor can also be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Lys (DYKDDDDK) (**SEQ ID NO: 8**) (Hopp et al., Bio/Technology 6:1204,1988.) The latter sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. This sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing. Fusion proteins capped with this peptide may also be resistant to intracellular degradation in E. coli.

Please delete the paragraph on page 34, line 22, to page 35, line 3 and replace it with the following paragraph:

(2) Information for SEQ ID No:4: (amino acid sequence of human immunoglobulin Fc fragment)

- (i) Sequence characteristics: (A) Length: 23[[2]] amino acids; (B) Type: amino acid; (C) Topology: linear.
- (ii) Molecular type: protein.
- (iii) Sequence description: SEQ ID No:4: (amino acid sequence of human immunoglobulin Fc fragment)

EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS  
CSVMHEALHNHYTQKSLSLSPG